AMENDMENTS TO THE SPECIFICATION

Amend the paragraphs beginning on page 46, line 20, and ending on page 47, line 12, as follows:

2. Summary and Conclusions:

All five antibodies showed different profiles in the PepSpot analysis. A schematic summary is given in Fig. 7, which illustrates the different aa sequences of CD38 being recognized. The epitope for MOR03079 and chimeric OKT10 can clearly be considered as linear. The epitope for MOR03079 can be postulated within aa 192 – 206 (VSRRFAEAACDVVHV **(SEQ ID NO:38)**) of CD38 whereas for chimeric OKT10 a sequence between aa 284 and 298 (FLQCVKNPEDSSCTS **(SEQ ID NO:39)**) is recognized predominantly. The latter results confirm the published data for the parental murine OKT10 (Hoshino *et al.*, 1997), which postulate its epitope between aa 280-298. Yet, for a more precise epitope definition and determination of key amino acids (main antigen-antibody interaction sites) a shortening of peptides VSRRFAEAACDVVHV **(SEQ ID NO:38)** and FLQCVKNPEDSSCTS **(SEQ ID NO:39)** and an alanine-scan of both should be envisaged.

The epitopes for MOR03080 and MOR03100 can be clearly considered as discontinuous since several peptides covering different sites of the protein sites were recognized. Those peptides comprise aa 82-94 and aa 158-170 for MOR03080 and aa 82-94, 142-154, 158-170, 188-200 and 280-296 for MOR03100. However, some overlaps between both epitopes can be postulated since two different sites residing within aa positions 82-94 (CQSVWDAFKGAFI **(SEQ ID NO:40)**; peptide #20) and 158-170 (TWCGEFNTSKINY **(SEQ ID NO:41)**; peptide #58) are recognized by both antibodies.